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gcaccaa	acc a M	tg go	cc a la Ti	cg t hr P	tt gi he Va 5	tg ga	ag c lu L	tc a eu S	gt ad er Tl	cc a hr Ly 1	aa g ys A	cc a la L	ag a ys M	tg cco et Pro	2 111
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gcaccaa att gtg Ile Val	agc a Mo 1	tg go et Al	cc a la Ti	cg t hr P act Thr	tt gi he Va 5 tgg	tg ga al G	ag c lu L	tc a eu S	gt a er Tl ctc Leu	cc achr Li	aa g ys A O aaa	cc a la L	ag a ys Mo	tg cco et Pro gaa Glu	2 111
caaaaaa gcaccaa att gtg	agc a Mo 1	tg go et Al	cc a la Ti	cg t hr P	tt gi he Va 5 tgg	tg ga al G	ag c lu L	tc a eu S	gt ader Ti	cc achr Li	aa g ys A O aaa	cc a la L	ag a ys Mo	tg cco et Pro gaa	2 111
gcaccaa gcaccaa att gtg Ile Val	eage M 1 g ggc	tg go et A ctg Leu	cc adla Ti ggc Gly	cg t hr Ph act Thr 20	tt gi he Va 5 tgg Trp	tg ga al G aag Lys	ag c lu L tct Ser	tc a eu S cct Pro	gt acer Tl	cc a hr L 1 ggc Gly	aa g ys A O aaa Lys	cc a la L gtg Val	ag a ys M aaa Lys	tg cco et Pro gaa Glu 30	111
gcaccaa att gtg Ile Val 15	acc a Mi 1 g ggc Gly	tg go et A ctg Leu gtg	cc adla Ti	eg thr Phase act Thr 20	tt gi he Va 5 tgg Trp gat	tg gal G	ag c lu L tct Ser	tc a eu S cct Pro	gt acer Ti	ggc Gly	aa g ys A O aaa Lys	cc adla Lygtg yal	ag a ys M aaa Lys tgt	gaa Glu gcc	2 111
gcaccaa gcaccaa att gtg Ile Val	acc a Mi 1 g ggc Gly	tg go et A ctg Leu gtg	ggc Gly gcc Ala	eg thr Phase act Thr 20 att	tt gi he Va 5 tgg Trp gat	tg gal G	ag c lu L tct Ser	tc aceu S cct Pro tat Tyr	gt acer Ti	ggc Gly	aa g ys A O aaa Lys	cc adla Lygtg yal	ag a ys M aaa Lys tgt Cys	gaa Glu gcc	111
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att gtg Ile Val 15 gca gtg Ala Val	age acc a Miles age acc a Miles age acc a acc acc acc acc acc acc acc acc	ctg Leu gtg Val	ggc Gly gcc Ala 35	act Thr 20 att Ile	tt gi he Va tgg Trp gat Asp	aag Lys gca Ala	ag c lu L tct Ser gga Gly	tc act Pro	gt acer Ti	ggc Gly cac His	aa g ys A O aaa Lys att Ile	gtg Val gac Asp	ag a ys Mo aaa Lys tgt Cys 45	gaa Glu 30 gcc Ala	111
gcaccaa att gtg Ile Val 15 gca gtg Ala Val	age acc a Miles age acc a Miles age acc a acc acc acc acc acc acc acc acc	ctg Leu gtg Val	ggc Gly gcc Ala 35	act Thr 20 att Ile	tt gi he Va tgg Trp gat Asp	aag Lys gca Ala	ag c lu L tct Ser gga Gly gtg Val	tc act Pro	gt acer Ti	ggc Gly cac His	aa g ys A O aaa Lys att Ile	gtg Val gac Asp	ag a ys Mo aaa Lys tgt Cys 45	gaa Glu 30 gcc Ala	207
att gtg Ile Val 15 gca gtg Ala Val	age acc a Miles age acc a Miles age acc a acc acc acc acc acc acc acc acc	ctg Leu gtg Val	ggc Gly gcc Ala 35	act Thr 20 att Ile	tt gi he Va tgg Trp gat Asp	aag Lys gca Ala	ag c lu L tct Ser gga Gly	tc act Pro	gt acer Ti	ggc Gly cac His	aa g ys A O aaa Lys att Ile	gtg Val gac Asp	ag a ys Mo aaa Lys tgt Cys 45	gaa Glu 30 gcc Ala	207
att gtg Ile Val 15 gca gtg Ala Val tat gtc	age  M  1  1  1  1  2  3  3  4  4  5  6  1  1  1  1  1  1  1  1  1  1  1  1	ctg Leu gtg Val cag Gln 50	ggc Gly gcc Ala 35 aat Asn	act Thr 20 att Ile gaa Glu	tt gi he Vi tgg Trp gat Asp	aag Lys gca Ala gaa Glu	ag c lu L tct ser gga Gly gtg Val 55	cct Pro tat Tyr 40 ggg Gly	gt acer The ctc Leu 25 cgg Arg	ggc Gly cac His	aa g ys A O aaa Lys att Ile atc	gtg Val gac Asp caa Gln 60	ag a ys Mo aaa Lys tgt Cys 45 gag Glu	gaa Glu 30 gcc Ala aag	207 255
att gtg Ile Val 15 gca gtg Ala Val tat gtc Tyr Val	age  M  1  1  1  1  1  1  1  1  1  1  1  1	ctg Leu gtg Val cag Gln 50	ggc Gly gcc Ala 35 aat Asn	act Thr 20 att Ile gaa Glu	tt gi he Vi tgg Trp gat Asp cat His	aag Lys gca Ala gaa Glu	ag c lu L tct ser gga Gly gtg Val 55	tc aceu S cct Pro tat Tyr 40 ggg Gly	gt acer Ti	ggc Gly cac His	aa g ys A O aaa Lys att Ile atc	gtg Val gac Asp caa Gln 60	ag a ys Mo aaa Lys tgt Cys 45 gag Glu agc	gaa Glu 30 gcc Ala aag Lys	207
att gtg Ile Val 15 gca gtg Ala Val tat gtc	agc a M 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ctg Leu gtg Val cag Gln 50	ggc Gly gcc Ala 35 aat Asn	act Thr 20 att Ile gaa Glu	tt gi he Vi tgg Trp gat Asp cat His	aag Lys gca Ala gaa Glu cgg	ag c lu L tct ser gga Gly gtg Val 55	tc aceu S cct Pro tat Tyr 40 ggg Gly	gt acer Ti	ggc Gly cac His	aa g ys A aaa Lys att Ile atc Ile	gtg Val gac Asp caa Gln 60	ag a ys Mo aaa Lys tgt Cys 45 gag Glu agc	gaa Glu 30 gcc Ala aag Lys	207 255
att gtg Ile Val 15 gca gtg Ala Val tat gtc Tyr Val	age  M  1  1  1  1  1  1  1  1  1  1  1  1	ctg Leu gtg Val cag Gln 50	ggc Gly gcc Ala 35 aat Asn	act Thr 20 att Ile gaa Glu	tt gi he Vi tgg Trp gat Asp cat His	aag Lys gca Ala gaa Glu	ag c lu L tct ser gga Gly gtg Val 55	tc aceu S cct Pro tat Tyr 40 ggg Gly	gt acer Ti	ggc Gly cac His	aa g ys A O aaa Lys att Ile atc	gtg Val gac Asp caa Gln 60	ag a ys Mo aaa Lys tgt Cys 45 gag Glu agc	gaa Glu 30 gcc Ala aag Lys	207 255
att gto Ile Val 15 gca gto Ala Val tat gto Tyr Val atc caa Ile Gln	age Acc a M 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ctg Leu gtg Val cag Gln 50 aag Lys	ggc Gly gcc Ala 35 aat Asn	act Thr 20 att Ile gaa Glu gtg Val	tt gi he Va tgg Trp gat Asp cat His	aag Lys gca Ala gaa Glu cgg Arg	ag c lu L tct ser gga Gly gtg Val 55 gag Glu	tc aceu S cct Pro tat Tyr 40 ggg Gly gac Asp	gt acer Tl	ggc Gly cac His	aa g ys A aaa Lys att Ile atc Ile 75	gtg Val gac Asp caa Gln 60 gtc	ag a ys Mo aaa Lys tgt Cys 45 gag Glu agc Ser	gaa Glu 30 gcc Ala aag Lys	207 255 303
att gtg Ile Val 15 gca gtg Ala Val tat gtc Tyr Val atc caa Ile Gln	age	ctg Leu gtg Val cag Gln 50 aag Lys	ggc Gly gcc Ala 35 aat Asn gct Ala	act Thr 20 att Ile gaa Glu gtg Val	tt gi he Vi tgg Trp gat Asp cat His aag Lys	aag Lys gca Ala gaa Glu cgg Arg 70	ag c lu L tct Ser gga Gly gtg Val 55 gag Glu agc	tc aceu S cct Pro tat Tyr 40 ggg Gly gac Asp	gt acer Tl	ggc Gly cac His	aa g ys A aaa Lys att Ile atc Ile 75	gtg Val gac Asp caa Gln 60 gtc	ag a ys Mo aaa Lys tgt Cys 45 gag Glu agc Ser	gaa Glu 30 gcc Ala aag Lys	207 255
att gto Ile Val 15 gca gto Ala Val tat gto Tyr Val atc caa Ile Gln	age	ctg Leu gtg Val cag Gln 50 aag Lys	ggc Gly gcc Ala 35 aat Asn gct Ala	act Thr 20 att Ile gaa Glu gtg Val	tt gi he Vi tgg Trp gat Asp cat His aag Lys	aag Lys gca Ala gaa Glu cgg Arg 70	ag c lu L tct Ser gga Gly gtg Val 55 gag Glu agc	tc aceu S cct Pro tat Tyr 40 ggg Gly gac Asp	gt acer Tl	ggc Gly cac His	aa g ys A aaa Lys att Ile atc Ile 75	gtg Val gac Asp caa Gln 60 gtc	ag a ys Mo aaa Lys tgt Cys 45 gag Glu agc Ser	gaa Glu 30 gcc Ala aag Lys	207 255 303

tataaaccag	tgactaacca	ggttgagtgt	cacccatacc	tcacgcagga	gaaactgatc	413
cagtactgcc	actccaaggg	catcaccgtt	acggcctaca	gccccctggg	ctctccggat	473
agaccttggg	ccaagccaga	agaccettee	ctgctggagg	atcccaagat	taaggagatt	533
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gactttaaat	tgagtgatga	ggagatggca	accatactca	gcttcaacag	aaactggagg	713
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ctccactcat	gtcccatttt	agccaagctt	atttaagatc	acagtgaact	tagtcctgtt	893
atagacgaga	atcgaggtgc	tgttttagac	atttatttct	gtatgttcaa	ctaggatcag	953
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aaaaaaataa	taatcat					1090

<210> 2

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<211> .88

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val 20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val 35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln 50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp

65 70 75 80

Pro Thr Ser Arg Ser Arg Ser Ser 85

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gcaco	caa				_	_		_		-		ys A		_	tg ccc et Pro	111
att g Ile V 15			_				-								-	159
gca g Ala V		_		_		-	_						_	_	_	207
tat <u>c</u> Tyr V																255
atc o			_	_		_			_	_			_	_	_	303
ttg t Leu T							_						-			351
aag a Lys T 95																399
cac t His T			_			_			_	_					•	447

Asp Lys Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp  130  135  140	495
gag gcc atg gag gag ctg gtg gat gag ggg ctg gtg aaa gcc ctt ggg Glu Ala Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly 145 150 155	543
gtc tcc aat ttc agc cac ttc cag atc gag aag ctc ttg aac aaa cct Val Ser Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro 160 165 170	591
gga ctg aaa tat aaa cca gtg act aac cag gtt gag tgt cac cca tac Gly Leu Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr 175	639
ctc acg cag gag aaa ctg atc cag tac tgc cac tcc aag ggc atc acc Leu Thr Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr 195 200 205	687
gtt acg gcc tac agc ccc ctg ggc tct ccg gat aga cct tgg gcc aag Val Thr Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys 210 215 220	735
cca gaa gac cct tcc ctg ctg gag gat ccc aag att aag gag att gct Pro Glu Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala 225 230 235	783
gca aag cac tcc cca agt ctg tgacaccagc acgcattgtt gagaacattc Ala Lys His Ser Pro Ser Leu 240 245	834
aggtetttga etttaaattg agtgatgagg agatggeaac eataeteage tteaacaga	a 894
actggaggge ctgtaacgtg ttgcaatect ctcatttgga agactatece ttegatgeag	g 954
aatattgagg ttgaatctcc tggtgagatt atacaggaga ttctctttct tcgctgaag	1014
gtgactacct ccactcatgt cccattttag ccaagcttat ttaagatcac agtgaactta	a 1074
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aggatcagaa tatcacagaa aagcatggct tgaataagga aatgacaatt ttttccactt	1194
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gatcaataaa aaaaataata atcat	1279

<210> 4

<211> 245

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

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<223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val 1 5 10 15

Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val 35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln 50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp 65 70 75 80

Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr 85 90 95

Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp
100 105 110

Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys 115 120 125

Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala 130 135 140

Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu 165 170 175

Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr
180 185 190

Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr

195 200 205

Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu 210 215 220

Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys 225 230 235 240

His Ser Pro Ser Leu 245

<210> 5

<211> 1337

<212> DNA

<213> HOMO SAPIEN

<220>

<223> HUMAN ARL GENE

<400> 5

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ctgggcactt	ggaagtctcc	tctcggcaaa	gtgaaagaag	cagtgaaggt	ggccattgat	180
gcaggatatc	ggcacattga	ctgtgcctat	gtctatcaga	atgaacatga	agtggggaa	240
gccatccaag	agaagatcca	agagaaggct	gtgaagcggg	aggacctgtt	catcgtcagc	300
aagttgtggc	ccactttctt	tgagagaccc	cttgtgagga	aagcctttga	gaagaccctc	360
aaggacctga	agctgagcta	tctggacgtc	tatcttattc	actggccaca	gggattcaag	420
tctggggatg	accttttccc	caaagatgat	aaaggtaatg	ccatcggtgg	aaaagcaacg	480
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gactttaaat	tgagtgatga	ggagatggca	accatactca	gcttcaacag	aaactggagg	960
gcctgtaacg	tgttgcaatc	ctctcatttg	gaagactatc	ccttcgatgc	agaatattga	1020
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ctccactcat ·	gtcccatttt	agccaagctt	atttaagatc	acagtgaact	tagtcctgtt	1140
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aatatcacag	aaaagcatgg	cttgaataag	gaaatgacaa	ttttttccac	ttatctgatc	1260
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aaaaaaataa	taatcat					1380

<210> 6

- <211> 316
- <212> PRT
- <213> HOMO SAPIEN
- <220>
- <223> AMINO ACID SEQUENCE ENCODED BY HUMAN ARL GENE
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- Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val 20 25 30
- Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val 35 40 45
- Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln 50 55 60
- Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp 65 70 75 80
- Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr 85 90 95
- Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp
  100 105 110
- Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys
  115 120 125
- Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala 130 135 140
- Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser 145 150 155 160
- Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu 165 170 175
- Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr 180 185 190
- Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr 195 200 205
- Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu 210 215 220

Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys 225 230 235 240

His Lys Lys Thr Ala Ala Gln Val Leu Ile Arg Phe His Ile Gln Arg 245 250 255

Asn Val Ile Val Ile Pro Lys Ser Val Thr Pro Ala Arg Ile Val Glu 260 265 270

Asn Ile Gln Val Phe Asp Phe Lys Leu Ser Asp Glu Glu Met Ala Thr 275 280 285

Ile Leu Ser Phe Asn Arg Asn Trp Arg Ala Cys Asn Val Leu Gln Ser 290 295 300

Ser His Leu Glu Asp Tyr Pro Phe Asp Ala Glu Tyr 305 310 315